Resource Summary Report

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SYGNAL

RRID:SCR_023080
Type: Tool

Proper Citation

SYGNAL (RRID:SCR_023080)

Resource Information

URL: https://github.com/plaisier-lab/sygnal

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Description: Software pipeline to integrate correlative, causal and mechanistic inference approaches into unified framework that systematically infers causal flow of information from mutations to TFs and miRNAs to perturbed gene expression patterns across patients. Used to decipher transcriptional regulatory networks from multi-omic and clinical patient data. Applicable for integrating genomic and transcriptomic measurements from human cohorts.

Synonyms: SYstems Genetic Network AnaLysis

Resource Type: software toolkit, software resource

Defining Citation: PMID:27426982

Keywords: Integrating genomic and transcriptomic measurements, human cohorts, transcriptional regulatory networks, integrate correlative, causal and mechanistic inference, unified framework, infers causal flow of information, mutations to TFs, miRNAs to perturbed gene expression patterns across patients,

Funding: NIGMS P50GM076547;
NIGMS R01GM077398;
NSF ABI NSF-1262637;
NSF DBI-0640950;
NCI U24CA143835;
American Cancer Society Research Scholar Grant

Availability: Free, Available for download, Freely available

Resource Name: SYGNAL

Resource ID: SCR_023080

Record Creation Time: 20221229T050156+0000

Record Last Update: 20260729T044551+0000

Ratings and Alerts

No rating or validation information has been found for SYGNAL.

No alerts have been found for SYGNAL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Striker SS, et al. (2023) Systematic integration of protein-affecting mutations, gene fusions, and copy number alterations into a comprehensive somatic mutational profile. Cell reports methods, 3(4), 100442.